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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=10; day=20; hr=8; min=41; sec=57; ms=621;]

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Application No: 10771695 Version No: 2.0

Input Set:

Output Set:

Started: 2008-09-16 15:39:43.541
Finished: 2008-09-16 15:39:47.792
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 251 ms
Total Warnings: 13
Total Errors: 108
No. of SeqIDs Defined: 37
Actual SeqID Count: 37

Error code	Error Description
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141>
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
E 300	Invalid codon found Phe SEQID (3) POS: 97

Input Set:

Output Set:

Started: 2008-09-16 15:39:43.541
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Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 251 ms
Total Warnings: 13
Total Errors: 108
No. of SeqIDs Defined: 37
Actual SeqID Count: 37

Error code	Error Description
E 300	Invalid codon found Phe SEQID (3) POS: 100
E 300	Invalid codon found Ala SEQID (3) POS: 103
E 300	Invalid codon found Ser SEQID (3) POS: 106
E 300	Invalid codon found Pro SEQID (3) POS: 109
E 300	Invalid codon found Arg SEQID (3) POS: 112
E 300	Invalid codon found Ser SEQID (3) POS: 115
E 300	Invalid codon found Ala SEQID (3) POS: 118
E 300	Invalid codon found Gly SEQID (3) POS: 121
E 300	Invalid codon found Arg SEQID (3) POS: 124
E 300	Invalid codon found Lys SEQID (3) POS: 127
E 300	Invalid codon found Ile SEQID (3) POS: 130
E 300	Invalid codon found Glu SEQID (3) POS: 133
E 300	Invalid codon found Phe SEQID (3) POS: 136
E 300	Invalid codon found Arg SEQID (3) POS: 139
E 300	Invalid codon found Gly SEQID (3) POS: 142
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (4)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (8)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

Input Set:

Output Set:

Started: 2008-09-16 15:39:43.541
Finished: 2008-09-16 15:39:47.792
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 251 ms
Total Warnings: 13
Total Errors: 108
No. of SeqIDs Defined: 37
Actual SeqID Count: 37

Error code	Error Description
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (12)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (19)
E 320	Wrong Nucleic Acid Designator, ct in SEQID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)

SEQUENCE LISTING

<110> Hanke, Paul D.

Li D'Elia, Lhing Yew

Rayapati, John

Crafton, Corey

Walsh, Holly

<120> Increased Lysine Production by Gene Amplification

<130> 1533.1030002

<140> 10771695

<141> 2004-02-04

<150> 09/722, 441

<151> 2000 11 28

<150> US 60/173, 707

<151> 1999-12-30

<150> US 60/184, 130

<151> 2000-02-22

<160> 37

<170> PatentIn version 3.0

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<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

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Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat 144
Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt 192
Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

gtc gcc atg gct att gag tcc ctt ggc gca gaa gct caa tct ttc act 288
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc 336
Gly Ser Gln Ala Gly Val Leu Thr Glu Arg His Gly Asn Ala Arg
100 105 110

att gtt gac gtc aca ccg ggt cgt gtg cgt gaa gca ctc gat gag ggc 384
Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

aag atc tgc att gtt gct ggt ttt cag ggt gtt aat aaa gaa acc cgc 432
Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

gat gtc acc acg ttg ggt cgt ggt tct gac acc act gca gtt gcg 480
Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt 528
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag 576
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys

180	185	190	
ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly			624
195	200	205	
tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn			672
210	215	220	
gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu			720
225	230	235	240
att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr			768
245	250	255	
ggt gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile			816
260	265	270	
tcc gat aag cca ggc gag gct gcc aag gtt ttc cgt gcg ttg gct gat Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp			864
275	280	285	
gca gaa atc aac att gac atg gtt ctg cag aac gtc tcc tct gtg gaa Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu			912
290	295	300	
gac ggc acc acc gac atc acg ttc acc tgc cct cgc gct gac gga cgc Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg			960
305	310	315	320
cgt gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr			1008
325	330	335	
aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala			1056
340	345	350	
ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu			1104
355	360	365	
cgc gat gtc aac gtg aac atc gaa ttg att tcc atc tct gag atc cgc Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg			1152
370	375	380	
att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala			1200
385	390	395	400
ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr			1248

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420			
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20	25	30	
Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp			
35	40	45	
Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg			
50	55	60	
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu			
65	70	75	80
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr			
85	90	95	
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg			
100	105	110	
Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly			
115	120	125	
Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg			
130	135	140	
Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala			
145	150	155	160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
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<210> 3

<211> 1035

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1035)

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atg cgc acc ttt ttg gaa gag cgc aat ttc cca gct gac act gtt cgt 96
Met Arg Thr Phe Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg
20 25 30

ttc ttt gct tcc ccg cgt tcc gca ggc cgt aag att gaa ttc cgt ggc 144
Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly

35 40 45

acg gaa atc gag gta gaa gac att act cag gca acc gag gag tcc ctc 192
Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
50 55 60

aag ggc atc gac gtt gcg ttg ttc tct gct gga ggc acc gct tcc aag 240
Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
65 70 75 80

cag tac gct cca ctg ttt gct gct gca ggc gcg act gtt gtg gat aac 288
Gln Tyr Ala Pro Leu Phe Ala Ala Gly Ala Thr Val Val Asp Asn
85 90 95

tct tct gct tgg cgc aag gac gac gag gtt cca cta atc gtc tct gag	336		
Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu			
100	105	110	
gtg aac cct tcc gac aag gat tcc ctg gtc aag ggc att att gcg aat	384		
Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn			
115	120	125	
cct aac tgc acc acc atg gct gca atg cca gtg ctg aag cca ctg cac	432		
Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His			
130	135	140	
gat gcc gct ggt ctt gta aag ctt cac gtt tcc tct tac cag gct gtt	480		
Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val			
145	150	155	160
tcc ggt tct ggt ctt gca ggt gtg gaa acc ttg gca aag cag gtt gct	528		
Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala			
165	170	175	
gca gtt ggc gac cac aac gtt gag ttc gtc cat gat gga cag gct gct	576		
Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala			
180	185	190	
gac gca ggc gat gtc gga cct tac gtt tcc cca atc gct tac aac gtg	624		
Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val			
195	200	205	
ctg cca ttc gcc gga aac ctc gtc gat gac ggc acc ttc gaa acc gac	672		
Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp			
210	215	220	
gaa gag cag aag ctg cgc aac gaa tcc cgc aag att ctc ggc ctc cca	720		
Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro			
225	230	235	240
gac ctc aag gtc tca ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc	768		
Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly			
245	250	255	
cac acg ctg acc att cac gcc gaa ttc gac aag gca atc acc gtc gag	816		
His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu			
260	265	270	
cag gcg cag gag atc ttg ggt gcc gct tca ggc gtc gag ctt gtc gac	864		
Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp			
275	280	285	
gtc cca acc cca ctt gca gct gcc ggc att gac gaa tcc ctc gtt gga	912		
Val Pro Thr Pro Leu Ala Ala Gly Ile Asp Glu Ser Leu Val Gly			
290	295	300	
cgc atc cgt cag gac tcc act gtc gac aac cgc ggt ctg gtt ctc	960		
Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu			
305	310	315	320

gtc gta tct ggc gat aac ctt cgc aag ggc gca gca ctg aac acc att 1008
Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile
325 330 335

cag att gct gag ctg ctg gtt aag taa 1035
Gln Ile Ala Glu Leu Leu Val Lys
340

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<211> 344

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 4

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20 25 30

Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly
35 40 45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
50 55 60

Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
65 70 75 80

Gln Tyr Ala Pro Leu Phe Ala Ala Gly Ala Thr Val Val Asp Asn
85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
100 105 110

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn
115 120 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
130 135 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val
145 150 155 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
165 170 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala
180 185 190

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val
195 200 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
210 215 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
225 230 235 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
245 250 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu
260 265 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Va